

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAAGCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTG
GCTTGTCCATCTCCCTCCGGGGGAGCGCGCGCTCCACCTTTGCCGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAAGCTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTAAACACTTCTTTTCCTTCTCTTCCCTCGTTTGGATTGCACCGCTTTCCA
TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGCCATCGT
CCATCTGGCTTATAAAAGTTTGTGAGCGCAGTCCAGAGGGCTGCGCTGCTGCTCCCTCGG
CTGGCAGAAGGGGTGACGCTGGGCAGCGCGAGGAGCGCGCGCTCGCTCTGGCGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG
TTGCACCATGCTCTTGTGATCGGGCTGTGATTCTTCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCCGCGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCGCCAGGCGTACGCTGCC
AAGGGATTACGCTGGCGGACATCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTGTGCGCACCACTTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTAGAAGTCTTCCAGGACCTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCCTGGAACGGATGTTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAAATACACTGACCAGCTCAAGCCATTGGAGACGTGCCCC
GGAACCTGAAGATTAGGTTACCCGCGCTTCTATGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGGGGGCTTCCCACTGTGAGGGCCCTGCA
ACAACTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCTGCAAGGCTCTTTCAGGGATGTGGTCAGCCCCAAACCTGCTCAGCC
CTCAGATCTGCCGCTCAGCTCCTGAAAATTTTAAATACAGTTTCAGGCCCTACAATCCTGA
GGAAGACCAACACTGCTGCGAGGCAACAAGCTTGGACCGGCTGGTCAGACAGATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGCTGTGTCAGCATTACCTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACAGATCAACAATCCGAGGTGGATGTGGACA
TCACTCGGCCGTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAACGGCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGAGATGGCAGTGGGTGCATGGATGACGTGTGTCCACCGGAGTTTGAAGTTTGTACCA
CAGAGGCCCCGCGAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCCAGCGTGGC
CACTCCCTGCTCTCTGGTCTCTCACTGCAATTGCTCTGGCACTGCAGAGACTGTGCAGATA
ATCTCTGGGTTTTTGGTCAGATGAACTGCATTTAGCTATCTGAATGGCCAACTCACTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCCTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCCTCCCTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG
CTTCTCTCTTCTTCTCAGCTTATCTGTGGGGACCTTGTTTATCTAGAGAGAATTCTTACTCAA
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTGTCTTTATGCTGCAGAAGTAAAGGAAT
CTCAGTTGTGAGGGTTTTTTTTTCTCATTAAAAAT

09973295.101501

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADV KARSCEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGLMYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHISKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

007323.4130

[illegible][illegible]